

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 05:44:19 ; Search time 43.44 Seconds
(without alignments)
922.506 Million cell updates/sec

Title: US-09-652-292-2
Perfect score: 2765
Sequence: 1 MGHSPVPICASVSLGGL.....CHRONSTGIPYSRIEISAAS 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT.*
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3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	20.5	526	20 AAY02168	A facilitative glu
2	556	20.1	629	22 AAB66935	Human GLUTX2. Hom
3	556	20.1	629	22 AAB66940	GLUTX2 consensus s
4	543	19.6	618	22 AAB66936	Rat GLUTX2. Rattu
5	541	19.6	582	21 AAG29528	Arabidopsis thalia
6	536.5	19.4	555	21 AAG29529	Arabidopsis thalia
7	517.5	18.7	480	22 AAM00107	Sugar transporter
8	507	18.3	551	20 AAY50799	Spinach glucose tr
9	506	18.3	478	21 AAG15416	Arabidopsis thalia
10	506	18.3	493	21 AAG15415	Arabidopsis thalia
11	506	18.3	546	21 AAG15414	Arabidopsis thalia

12	504	18.2	491	21 AAB12594	Brevibacterium lac
13	502	18.2	491	22 AAG89949	C glutamicum prote
14	500.5	18.1	518	20 AAY49632	Soybean hexose car
15	488.5	17.7	522	21 AAG52315	Arabidopsis thalia
16	482.5	17.5	522	21 AAG16798	Arabidopsis thalia
17	479	17.3	491	21 AAG52316	Arabidopsis thalia
18	478	17.3	477	22 AAE04888	Human transporter
19	475	17.2	508	21 AAG29530	Arabidopsis thalia
20	474.5	17.2	478	22 AAB66933	Rat GLUTX1. Rattu
21	473	17.1	491	21 AAG16799	Arabidopsis thalia
22	470	17.0	477	22 AAB66932	Human GLUTX1. Hom
23	466.5	16.9	491	21 AAG32072	Arabidopsis thalia
24	466.5	16.9	508	21 AAG32071	Arabidopsis thalia
25	465.5	16.8	478	22 AAB66939	GLUTX1 consensus s
26	460.5	16.7	507	22 AAB66941	GLUTX3 consensus s
27	460	16.6	473	21 AAG52317	Arabidopsis thalia
28	457.5	16.5	474	19 AAW58862	T. halophilus xyul
29	455	16.5	507	22 AAB66937	Human GLUTX3. Hom
30	454	16.4	473	21 AAG16800	Arabidopsis thalia
31	450	16.3	477	22 AAB66934	Murine GLUTX1. Mu
32	438.5	15.9	511	20 AAY49630	Rice hexose carrie
33	437	15.8	492	21 AAB13225	H17B01.1-GFP fusio
34	433.5	15.7	474	21 AAG50066	Arabidopsis thalia
35	429.5	15.5	466	21 AAG32073	Arabidopsis thalia
36	427	15.4	493	20 AAY27292	Glucose transporte
37	427	15.4	493	22 AAB30522	Amino acid sequenc
38	418.5	15.1	522	18 AAW17836	Rat glucose transp
39	417	15.1	517	20 AAY49633	Wheat hexose carri
40	414	15.0	508	22 AAG93128	C glutamicum prote
41	407.5	14.7	503	22 AAB66938	Rat GLUTX3. Rattu
42	407.5	14.7	509	20 AAY27290	Glucose transporte
43	404.5	14.6	494	20 AAY27289	Glucose transporte
44	397.5	14.4	415	21 AAG50067	Arabidopsis thalia
45	396.5	14.3	502	20 AAY49625	Corn hexose carrie

ALIGNMENTS

RESULT 1
AAY02168
ID AAY02168 standard; Protein; 526 AA.
XX
AC AAY02168;
XX
DT 08-JUL-1999 (first entry)
XX
DE A facilitative glucose transporter protein GLUT8.
XX
KW Facilitative glucose transporter protein; GLUT8; malignancy;
KW breast cancer; prostate cancer; epithelial cell cancer;
KW non-insulin-dependent diabetes mellitus; insulin resistance;
KW central obesity; hypertension; dyslipidaemia; glucose intolerance;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO9918125-A1.
XX
PD 15-APR-1999.
XX
PF 30-SEP-1998; 98WO-AU00819.
XX
PR 01-OCT-1997; 97AU-0009573.
XX
PA (SVIN-) ST VINCENT'S INST MEDICAL RES.
XX
PI Best JD, Rogers SD;
XX
DR WPI; 1999-277253/23.
DR N-PSDB; AAX35516.
XX
PT Nucleic acid encoding a facilitative glucose transporter

[illegible]

PR	27-AUG-1999;	9905-0151080;
PR	30-AUG-1999;	9905-0151303;
PR	31-AUG-1999;	9905-0151348;
PR	01-SEP-1999;	9905-0151930;
PR	07-SEP-1999;	9905-0152363;
PR	10-SEP-1999;	9905-0153070;
PR	13-SEP-1999;	9905-0153758;
PR	15-SEP-1999;	9905-0154018;
PR	16-SEP-1999;	9905-0154039;
PR	20-SEP-1999;	9905-0154779;
PR	22-SEP-1999;	9905-0155139;
PR	23-SEP-1999;	9905-0155486;
PR	24-SEP-1999;	9905-0155653;
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PR	25-OCT-1999;	9905-0161404;
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PR	28-OCT-1999;	9905-0161992;
PR	28-OCT-1999;	9905-0161993;
PR	29-OCT-1999;	9905-0162142;
PR	29-OCT-1999;	9905-0162143;

Query Match
Best Local Similarity
13.0%; Score 341; DB 41
28.8%; Pred. No. 1.3e-40;

13;

Qy	4	SPVPVPLCASVSLGLLFTGVYELAVISGALLPLQLDF---GLSCLBQEFVLVSGLLLGALL	60
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Qy	61	ASLVGGFLDTCYGRQATILGSLNLVLGAGSLTGLIAGSLAWLVIGRAVGVGPAISLSLMACC	120
Db	83	gaavggvwdnkIgrmsllldvdlIgalvmaIapspwvlvgrIvfgvgyvmasmtsp	140
Qy	121	IYVSELVGRQRGVLSVSYEAGITVGIILSYALNYALAGTPWGRHMFNGATAPAVLQSL	180
Db	143	lyIsesparIgaIvstngllIgtggffslylnIatvhtpgtwrmIvlgavgyvpaIvqv	200
Qy	181	SLILFLPAG-----TDETATHKDLIPLOGEAK-----LGPGR	210
Db	203	lmIsIpesprIyIrdIaesrallerIypadeveaeemealkI-sveaeKadeaIlg---	250
Qy	214	PRYSFLDLERAR-----DNNRGRTTVGLGLVLIFQOLTGQPNVLCYASTIFSSVGHGG	260
Db	259	-----dsIsakIcafnpvrIlaagIvlgavagcIvIvntvmvysvIsaIvafaaasn	310

QY 267 SSAVLASVGLGAVKVAATLTAMGLVDGRALL-----LACALMALSVSGILYSFA 320
 Db 313 ktamalslitsginalgsivmmfvdrygrkkmilmsfgiacililactvfsqaal-ha 371
 QY 321 VPMDSGPSCLAVPNATQOTGLPGDGLLOPSLPPIPTRTNEDOREPILSTAKTKPHPRS 380
 Db 372 pkidafesrtfapnatsayap-----laenapp-----srwcmkclirsecgfcas 419
 QY 381 G-DPSAPPRALSSALPCPLPARGHALLR-----WTALLCLAVFVSAFSGFGPVT 431
 Db 420 gvqpyapagacvvsddmkatcsgrtffkdgcpskfgflaivflgfyvvyapgmgtvp 479
 QY 432 WLVLSEIYPVEIRGARAFACNSFNWAANLFISLSFLDLICTIGLSWTFLLYGLTAVLGLG 491
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 Db 540 fiwllvpetkglgfeevk 558

RESULT 6

AG29529
 ID AG29529 standard; Protein: 555 AA.

AC AAG29529;

XX XX

DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 35151.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX XX 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

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PR 04-MAY-1999; 99US-0132407.

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PR 26-OCT-1999; 99US-0161361.
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 PR 28-OCT-1999; 99US-0161992.
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 PR 29-OCT-1999; 99US-0162142.
 Query Match 19.4%; Score 536.5; DB 21; Length 555;
 Best Local Similarity 28.9%; Pred. No. 3.2e-40;
 Matches 158; Conservative 88; Mismatches 225; Indels 75; Gaps 12;
 QY 17 LGGLTFEYELAVISGALLPLQLDF---GLSCLEQELVGLSLLGLGALLASLVGGFLIDCYG 73
 Db 9 igglfgydtgvisgalifkiedfdevdktkwlgstivmavagavgaavggwindkfg 68
 QY 74 RKOAILGSLNVLVLAGSLTGLAGSLAWLVGRVAVGFAISLSSMACCIYVSELVGRQRG 133
 Db 69 rmsliladwllfllgavmafapwvllvgrifvgvgmasmtsplylaesparirg 128
 QY 134 VLVSLEYAGITVGLILLSYALNYALAGTPWCRHMFGNATAPAVLQSLSLFLPAG---- 188
 Db 129 alvstngllitgqffsfylinlafvhtpgtwtmvgvavpaivqfvimisipesprwly 188
 QY 189 -----TDETATHKDLIPLQGGAPK-----LCPGRPRYSFLDLFRAR- 225
 Db 189 rkdrisrailleriypadeveamealkl-sveaeekadeaifg-----dsfsakl 238
 QY 226 -----DNMRGRTTVGLGLVLFQOLTGQPNVLCYASTIFSSVGFHGGSSAVLASVGLGAV 279
 Db 239 kgafgnpvvrrglaaigtvqvgvqfvgintvmyyspaivqfagyasnkamalslfcagl 298
 QY 280 KVAATLTAMCLVDRAGRALL-----LACALMALSVSGILVSVFVPMDSGSPCLAVP 333
 Db 299 nalgsivsmmfvdrygrkmlismfgitacililatvfsqaal-hapkidafesrtfap 357
 QY 334 NATGQTGLPGDSGLLQDSSLPPIPTNEDQREPILSAKTKPHPRSG-DPSAPPRLALS 392
 Db 358 natscayap-----laenapp-----srnckmrkrcsecfcagvapyagacvvl 405
 QY 393 SALPGPLPARGHALLR-----WTALLCLMVFSVSAFSGFGPVTMLVSEIYVVEIR 444
 Db 406 sddmkatcsgrgrtffkdgcpskfgflaivflgylvyvypgmgtvpwivnseiypryr 465
 QY 445 GRAFAPCNSFWAANLPISLFLDITGLTIGLTSWTFLLYGLTAVLGLCFIYLFVPEKQGS 504
 Db 466 glggtaavsnwvsnlivsesfslthalgsgsgtflfagfstglfllwlpvetkgql 525
 QY 505 LAEIDQ 510
 Db 526 feevek 531
 RESULT 7
 AAM00107
 ID AAM00107 standard; Protein; 480 AA.
 XX AAM00107;
 XX
 DT 28-SEP-2001 (first entry)
 XX
 DE Sugar transporter sequence #175.
 XX
 KW Moss; carbohydrate metabolism related protein; CNRP; sugar; cofactor;
 fine chemical production; carbohydrate; polysaccharide.
 XX
 OS Physcomitrella patens.
 XX
 PN WO20014476-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 14-DEC-2000; 2000MO-EP12697.
 XX
 PR 16-DEC-1999; 99US-0171101.


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Best Local Similarity 29.7%, Pred. No. 1.5e-37;
Matches 156; Conservative 72; Mismatches 191; Indels 106; Gaps 10:

Oy 4 SPPVLPACASVSLGGLTFGYELAVISGALLPQLDFGL--SCLQEFLVSGLLGALLA 61
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Db 107 sasvlpy-vgvaclgailfghylgvngaldylsadlalagntvlqgwwvslilagatvg 165
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Oy 62 SILVGGFLIDCGRKQAILGSLNVLVLAGSLTGLAGSLAWLVGRAVVGFAISLSSMACCI 121
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DT 17-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX
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KW termination sequence.
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OS Arabidopsis thaliana.
XX EP1033405-A2.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 26-OCT-1999; 99US-0161359.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 18.3%; Score 506; DB 21; Length 546;
 Best Local Similarity 29.5%; Pred. No. 1.8e-37;
 Matches 155; Conservative 68; Mismatches 196; Indels 106; Gaps 8;

QY 4 SPVPLCLASVSLGLTGYELAVISGALLPLQLDFGL--SCLEFELVGSLLGALLA 61
 DB 102 sgtvlpf-vgvaclgallfghyhgvgngaleyakldgiaentvlggwiwssilagatvg 160
 QY 62 SLVGGFLIDCYGRKQALGSLNLLAGSLTLGLAGSLAMVLGKAVVGVFAISLSSMACCI 121
 DB 161 sftggaladkfgrtrfqlidaifagfcatagvqtmivgrllagigigissalvpl 220
 QY 122 YVSELVGRQRGVLSLYEAGITVGVLLSYALNYALAGTPWGRHMFGWATAPAVLQSL 181
 DB 221 yiseisptelrgaelgsvnqflicigilaialagplaaaplwwrtmfgvavipsvllaig 280
 QY 182 LLPLPAGT-----DETAKHDLIPLOGGE-----APKLGPRPRYSFLDLFRA 224
 DB 281 mafspesprvlvqgkvseaeakltlygkervvelvrdlsasggqgssepegwdfdfs 340
 QY 225 RDNMRGRTTVGLVLFQOLGTGPNVLCYASTIFSSVGHGSSAVLASVGLGAVKVAAT 284
 DB 341 r--ykwsvgaalfifqlaglnavvyystsvfrsagi---qsdvaasalvgasnfvgt 395
 QY 285 LTAMGLVDRAGRALLAGCALMALSVGIGLVSAFVPMDSGSPCLAVPNATGOTGLPGD 344
 DB 396 avasslmdkmgrksllitstfggmalsm-----lllsftwkaaya 438
 QY 345 SGLQDSSLPPIPTNEDQREPLSTAKTKPHRSCDPSAPPRLALSSALPGPPLPARG 404
 DB 423 -----lllsftwkaaya 438
 QY 405 HALLRTALCLMVFVSFAFSFGPGVPTWLVSEIYPVEIRGAFACNCFNNAANLFLISL 464
 DB 439 gtl----avvgtyvlsfslgagvpalllpelfasrirakavalsgmhwnisnfvigl 494
 QY 465 SFDLTGITGLSWTFLLYGLTAVLGFTYLFVPTKGSGLAEID 509
 DB 495 yflsvvktfgisvylgfgavcvlavlylagnvvetkgrsleeie 539

RESULT 12
 AAB12594
 ID AAB12594 standard; Protein; 491 AA.
 AC AAB12594;
 XX
 XX
 DT 09-NOV-2000 (first entry)
 DE Brevibacterium lactofermentum sugar transporter protein SEQ ID NO:6.
 DE Brevibacterium lactofermentum; glcBD; sugar transporter; breeding;
 KW corynebacterium; phosphoenolpyruvate-sugar transport system; PTS;
 KW non-PTS.
 XX Brevibacterium lactofermentum.
 OS
 XX WO200037497-A1.
 PN
 XX 29-JUN-2000.
 PD
 XX 16-DEC-1999; 99WO-JP07078.
 PF
 XX 18-DEC-1998; 98JP-0360620.
 PR
 XX (AJTN) AJINOMOTO CO INC.
 PA
 XX Kanno S, Kimura E, Matsui K, Nakamatsu T;
 PI WPI; 2000-442642/38.
 XX DR N-PSDB; AAA65400.
 XX

PT Sugar transporter gene gltBD of Brevibacterium lactofermentum, useful
 PT for production of coryneform bacteria with altered membrane sugar
 PT transport
 XX
 XX Claim 1; Page 21-23; 26pp; Japanese.
 XX
 CC The present invention describes a protein which has a transmembrane sugar
 CC transport activity. The protein is specifically a non
 CC phosphoenolpyruvate-sugar transport system (PTS) sugar transporter.
 CC It can be used for in breeding corynebacteria with altered transmembrane
 CC sugar transport. The present represents the Brevibacterium lactofermentum
 CC sugar transporter encoded by the gltBD gene, which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 491 AA;
 SQ

Query Match 18.2%; Score 504; DB 21; Length 491;
 Best Local Similarity 26.5%; Pred. No. 2.4e-37;
 Matches 139; Conservative 87; Mismatches 190; Indels 108; Gaps 9;

QY 12 ASVSLGLGLTFGYELAVISGALLPLQLDFGLSCLEFELVGSLLGALLASLVGGFLIDC 71
 DB 33 alvatfgllfgdytdgvingalnptmreigltaftgvtssllfgaaagamffgrisdn 92
 QY 72 YGRKQAILGSNLVLLAGSLTLGLAGSLAMVLGKAVVGVFAISLSSMACCIYVSELVGRQ 131
 DB 93 wgrkrkllslavafvgtmvcvfapfvamvgrvllglavgastvpyyiaelapfel 152
 QY 132 RGVLSLYEAGITVGVLLSYALNYALAGTPWG-----WRHMFQWATAPAVLQSLFLP 186
 DB 153 rgslngrnelmivvgqlaafvln-alignvfhghdgwvrymlaalaipalalfgmrlvp 211
 QY 187 AG-----TDET-ATHKDLIPLOGGE-----PKLGPRPRYSFLDLFRARD 226
 DB 212 esprwlvgrgridearavletirplerahaevadvehlareehavseksmgilreilsskw 271
 QY 227 NMRGRTTVGLVLFQOLGTGPNVLCYASTIFSSVGHGSSAVLASVGLGAVKVAATLT 286
 DB 272 lvr-illvgiglgvaqqltginsimyygqvvlleaaf-senaalianavpgvliavvgafl 329
 QY 287 AMGLVDRAGRALLAGCALMALSVGIGLVSAFVPMDSGSPCLAVPNATGOTGLPGDSG 346
 DB 330 alwmmdrinrtrtlitgyslttishvligiaslafv----- 366
 QY 347 LLQDSSLPPIPTNEDQREPLSTAKTKPHRSCDPSAPPRLALSSALPGPPLPARGHA 406
 DB 367 -----gdlrp----- 372
 QY 407 LLRTWALLCLMVFVSFAFSFGPGVPTWLVSEIYPVEIRGAFACNCFNNAANLFLISL 466
 DB 373 ---yvltlvvfvsgmqfllnavatwmiselfplamrgfaigvsvffliwianafglff 429
 QY 467 LDLTIGTIGLWTFLLYGLTAVLGFTYLFVPTKGSGLAEIDQ 510
 DB 430 ptmeavglgtgffmfigavlgvvaliflyqvbetgrtleide 473

RESULT 13
 AAG89949
 ID AAG89949 standard; Protein; 491 AA.
 AC AAG89949;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 XX C glutamicum protein fragment SEQ ID NO: 3703.
 DE
 XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX Corynebacterium glutamicum.
 OS
 XX

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PN EP108790-A2.
XX
XX PD
XX PF
XX PP
XX PR
XX PR
XX PR
XX PR
XX PA
XX PI
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI: 2001-376931/40.
DR N-PSDB: AAH65168.
DR
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
XX Claim 17; SEQ ID NO: 3703; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a protein described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 491 AA;
Query Match 18.2%; Score 502; DB 22; Length 491;
Best Local Similarity 26.5%; Pred. No. 3.7e-37;
Matches 139; Conservative 87; Mismatches 190; Indels 108; Gaps 9
QY 12 ASVSLGGLTGYELAVISGALLPLQLDFGLSCLEQFLVGSLILGALLASLVGGFLIDC 71
Db ||| ||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | : |
33 alvatfggllfydgtvginalnptrlgitaftegvvtssallfgaagaamffgrisdn 92
QY 72 YGRKOALIGSNLVLLAGSLTLGLAGSLAWLVGRAVGFATLSLSMACCIYVSELVGPQR 131
Db ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
93 wgrktlislavaffgmicvfapsvmvvgrvllglavggastcvvpvytaelpafel 152
QY 132 RGVLSVLYEAGITVGILLSYALNALACTPMG-----WRHMFGMATAPAVLSLSLLFLP 186
Db || | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
153 rgsIagrnelmivvglaafvin-aIlgnvghdhgvrwrymlataipaiaIffgmIrvp 211
QY 187 AG-----TDET-ATHKDLIPLOGEA-----PKLGPRRPYSFLDLPFRARD 226
Db || | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
212 esprwlvergridraearvletirplehaevadvhehlarehavseksmgirellskw 271
QY 227 NMGRRTVTGLGLFLOOLTGQPNVLCYASTIFSSVFHGGSAAVLASVCLGAVKVAATLT 286
Db : | ||| : | |||| : | : | : | : | : | : | : | : | : | : | : |
272 lvr-IlIvlgIvgaqltgInsImyYqgvIIeaGf-senaalIatnavgpviavvgafi 329
QY 287 AMGLVDAGRALLAGCALMALSVGI GLVSFAVPMDSGSPSCLAVPNATGTGLPGDSG 346
Db | : ||| || : | : | : | : | : | : | : | : | : | : | : | : | : |
330 alwmmdrlnrrtlItgySlttshlvIgiaavfpv----- 366,
QY 347 LLQDSSLPPPTWNEDQREPLSTAKTKPHRSDGPSAPPRLASSLALPGPPLPARGHA 406
Db ||| |
367 -----gdplr----- 372

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Query Match					
Best Local Similarity 18.1%; Score 500.5; DB 20; Length 518;					
Matches 161; Conservative 81; Mismatches 196; Indels 145; Gaps 14;					
Oy	2	GHSPPVLPICASVSLLGLTTCGYELAVISG--ALLPLQLDFCLSCLEQE-----	48	PR	01-APR-1999;
Db	17	gsltftvtctvaamggllfydgldisggvtsmdpfllkffpsvrknksdktvnqycq	76	PR	06-APR-1999;
Oy	49	-----FLVGSLLLGALLASLVGGFLDCYGRKQAIILGSNLVLLAGSLTLGLAGSLAWL	101	PR	08-APR-1999;
Db	77	ydsqtltmftslylaallsslvastvrrfgrkxsmifglflfxgalingfaxhvwxl	136	PR	16-APR-1999;
Oy	102	VLGRAVGFATLSLMACCIIVSELVGPQRGVLSVLEAGITVGILLSYALNYALAGTP	161	PR	19-APR-1999;
Db	137	ivgrilllgfgrfnqsypvlxsmapkyrgalnigfqlstvgilvanvlnyfkakik	196	PR	21-APR-1999;
Oy	162	-WGRHMFEGWATAPAVLQSLSLLFLPAGTDETHAKDLIPLOGEAPKLGPGRPR----	215	PR	23-APR-1999;
Db	197	ggwgrlsglmgampallitvgsilvp-----dtpnsemiergdrekakaqlrigrdn	250	PR	28-APR-1999;
Oy	216	--YGFELDIFARDN-----MRGRTTVGLVLFGFQOLTGPNNVLCVASTIF	258	PR	30-APR-1999;
Db	251	vdeefndlvaasessqvhpwrnlrlqkrphltmavlipfqtlgtinvimfyapyvlf	310	PR	04-MAY-1999;
Oy	259	SSVGFHGSSAVLASVGLCAVKVAATLTAMGLVDNRAGRALLAGCALMALSVSGIGLVS	318	PR	05-MAY-1999;
Db	311	ssigfkd-daaalmsavitgvvvvatcvsiygvdkgwgralfleggvqmli-----	360	PR	06-MAY-1999;
Oy	319	FAPMDSGPCSLAVPNAT-----GOTGPLPGDSGLLODSSLPIPTNEDQRPILSTAKK	373	PR	07-MAY-1999;
Db	361	-----cqavvaaiaigakftgdgnpgd-----	381	PR	11-MAY-1999;
Oy	374	TKPHRGDPSPAPRRALSSALPGPPLPARGHALLRWTA---LCLMVFSAFSFGFGPV	430	PR	14-MAY-1999;
Db	382	-----lpkwyaiuvvficiyvsaafawswgpi	408	PR	14-MAY-1999;
Oy	431	TWLVLSEIYPVEIRGAPAFNCNSFNAAANLFISFLDLI--GTIGLSWTFLLYGLTAVL	488	PR	18-JUN-1999;
Db	409	gwlypseifpleirsaagsinvsnmflftllaqvflcmchmkfgl---flffaaffvli	465	PR	18-JUN-1999;
Oy	489	GLGFIYLFPVTKGSLAEIDQFKRRFTLSF-CHRONSWG I 530		PR	18-JUN-1999;
Db	466	mtfvvyflpeckplpteemgqvqwahpfwrfvehddyngnv	508	PR	18-JUN-1999;
RESULT 15					
ID	AAG52315	standard; Protein; 522 AA.		PR	18-JUN-1999;
AC	AAG52315;			PR	18-JUN-1999;
XX				PR	18-JUN-1999;
DT	18-OCT-2000	(first entry)		PR	18-JUN-1999;
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 66488.		PR	18-JUN-1999;
KW	Protein identification; signal transduction pathway; metabolic pathway;			PR	18-JUN-1999;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			PR	18-JUN-1999;
KW	termination sequence.			PR	18-JUN-1999;
OS	Arabidopsis thaliana.			PR	18-JUN-1999;
XX				PR	18-JUN-1999;
PN	EPI033405-A2.			PR	18-JUN-1999;
PD	06-SEP-2000.			PR	18-JUN-1999;
PF	25-FEB-2000; 2000EP-0301439.			PR	18-JUN-1999;
XX				PR	18-JUN-1999;
PR	25-FEB-1999;	99US-0121825.		PR	18-JUN-1999;
PR	05-MAR-1999;	99US-0123180.		PR	18-JUN-1999;
PR	09-MAR-1999;	99US-0123548.		PR	18-JUN-1999;
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PR	23-MAR-1999;	99US-0126785.		PR	18-JUN-1999;

PR	19-JUL-1999;	99US-0144331.
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PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
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PR	02-AUG-1999;	99US-0146388.
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PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
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PR	06-AUG-1999;	99US-0147303.
PR	09-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	10-AUG-1999;	99US-0148171.
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PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
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PR	18-AUG-1999;	99US-0149426.
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PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
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PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
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PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	06-OCT-1999;	99US-0157865.
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PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
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PR	22-OCT-1999;	99US-0160980.
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PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 17.7%; Score 488.5; DB 21; Length 522;		
Best Local Similarity 26.2%; Pred. No. 6.8e-36;		
Matches 155; Conservative 96; Mismatches 182; Indels 159; Gaps 17;		
Qy	4	SPVPLPCASVSLGGTFFGYELAVISCAL-LP--LQDFFGLSCLEQE----- 48
Db	20	tpvlfctcv-vaangglifdydigisgvtampsflkrffpsvyrkqgedastnqcyd 78
Qy	49	-----FLVGSLLGALLASLVGGFLIDCYGRKQATLGNLVLVLAGSLTGLAGSLAMLVL 103
Db	79	sptltmftsslylaalsslvastvtrkfrlamlfgllfcagalingfakhwmliv 138
Qy	104	GRAVVGFAISLSSMACCIYVSELVPGPRGVLSLYEAGITVIGILLSYALNALVAGTLP-- 161
Db	139	grillfglgfandavplylsemapykyrgalnlgfqlsiltigilvaevlnyffakikgg 198
Qy	162	WGRHMFQWATAPAVLOSLSLLFLP-----AGTDEATHKDLI 199
Db	199	wgrlslsggavvpallitigslvlpdtpnsmiergqheeaaklrirgvdvdeqefddi 258
Qy	200	PLQGEAPKLGPRPRYSFLDLFRARDNMGRRTTVGLVLVFLQQLTGQPNVLCYASTIFS 259
Db	259	vaakesqsi-----ehpwrnlrrk--yrphltmavmlpfqqlgtlnvimfyapvifn 311
Qy	260	SVGFHGGSSAVLASVGLGAVKVAATLTAKGLVDAGRALLAGCALMALSVSGICLVSP 319
Db	312	tlgfttdas-lmsavvtgsvnvvaatlvisygvdrwrrrflfledgtqmlf----- 360
Qy	320	AVPMDSGPSCIAVPNAT-----GQTGLPGDGLLQDSSLPPPTPTNEDQREPIILSTAKKT 374
Db	361	-----cqavvaacigakfgvdtgtpge----- 381
Qy	375	KHPRSGDPSAPPRIALSSALPGPLPARGHALLRWTALLC---LMVFVSASFSGFGVPT 431
Db	382	-----lpkwyalvvvtfcilvyagfawagpplg 409
Qy	432	WLVLSIYPVEIRGRAFCNSFNWAANLFLSLSPDLDLIGTI--GLSWTFLLYGLTAVLGL 489
Db	410	wlvpselplrsaaqslitvsvnmifftlaqifltlmlchlkfgl---flvafefvvvm 466
Qy	490	LGFTVLFVPETKGOSLAEIDQFOKR---RF-----TLSCFHCRONSTG 529
Db	467	slfyviflpetckgipieemgqvrshwywrsfvedgeygnalemgknqanqg 518

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